

SEQUENCE LISTING

<110> Tao, Yumin
Gordon-Kamm William J.
Lowe, Keith S.
Bailey, Matthew A.

<120> Cell Cycle Polynucleotide, Polypeptide,
and Uses Thereof

<130> 1109

<150> US 60/119,857

<151> 1999-02-12

<150> US 60/101,551

<151> 1998-09-23

<150> US 09/398,858

<151> 1999-09-20

<150> US 09/257,131

<151> 1999-02-25

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1636

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (109)...(1381)

<221> misc_feature

<222> (1)...(1636)

<223> n = A,T,C or G

<400> 1

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gccgatccgt cttcttcccc tcctctcgcg ggtcggcggt tggggatc atg gcg gcg      117
                                   Met Ala Ala
                                   1

cgg gcg gct gac gag aac agg aga ccg gcg gca ggg aag ccc gcg cca      165
Arg Ala Ala Asp Glu Asn Arg Arg Pro Ala Ala Gly Lys Pro Ala Pro
   5                               10                               15

ggc gtc cga gac atg gcg agc cgg cgc gcg ctc acg gac atc aag aac      213
Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp Ile Lys Asn
  20                               25                               30                               35

ctc gtc ggg gct gcc ccg tac ccc tac gcc gtc gcc aag aag ccc atg      261
Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys Lys Pro Met
                               40                               45                               50

ctg cag aag agc aaa agg gac gaa aag cag cca gcg ttg gca agc agc      309
Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu Ala Ser Ser

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aaa cag ctt gag cta gcg tca ttt ttc atg ctg gag ctc tgc ttg gta	1077
Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu Cys Leu Val	
310 315 320	
gaa tac caa atg ctg aat tat cgg cct tcg cat ctg gct gct gct gcg	1125
Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala Ala Ala Ala	
325 330 335	
gtt tat act gca cag tgt gct atc aat cgt tgc cag cac tgg aca aag	1173
Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His Trp Thr Lys	
340 345 350 355	
gtc tgc gag tct cat agc aga tac act agc gac caa ctc ctg gag tgc	1221
Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu Leu Glu Cys	
360 365 370	
tcg agg atg atg gta gat ttt cac cag aag gct gga acc agt aag ctc	1269
Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr Ser Lys Leu	
375 380 385	
act ggc gtg cac agg aag tac agt acc tac aag ttc ggt tgc gtg gcc	1317
Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly Cys Val Ala	
390 395 400	
aag att ttg cct gcg cag ttc ctg ctg gag tcg gga ggg aca ccg cct	1365
Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly Thr Pro Pro	
405 410 415	
cct tca ggt gca aac t agttgaatcg acctattcaa ctgggtggat tttttaaagt	1421
Pro Ser Gly Ala Asn	
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ttttagaata ctccatgaac aagatgcaga aaacatcgtg ttgatgttgc ccaaaagtgc	1481
atcgaatttc tttggagagt tatgattaac aacttttttt ttatctatgt tgaatgacga	1541
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<400> 2

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Pro Ala Pro Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp	
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Ile Lys Asn Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys	
35 40 45	
Lys Pro Met Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu	
50 55 60	
Ala Ser Ser Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser	
65 70 75 80	
Lys Gly Gln Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu	
85 90 95	
Val Cys Gln Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp	
100 105 110	
Val Glu Leu Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met	
115 120 125	
Gly Ala Thr Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met	
130 135 140	
Asp Ile Asp Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr	

145		150		155		160									
Val	Lys	Glu	Leu	Tyr	Thr	Phe	Tyr	Arg	Glu	Asn	Glu	Ala	Lys	Ser	Cys
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Val	Arg	Pro	Asp	Tyr	Met	Ser	Ser	Gln	Gln	Asp	Ile	Asn	Ser	Lys	Met
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Arg	Ala	Ile	Leu	Ile	Asp	Trp	Leu	Ile	Glu	Val	His	Tyr	Lys	Phe	Glu
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Leu	Glu	Lys	Glu	Val	Val	Pro	Arg	Lys	Lys	Leu	Gln	Leu	Val	Gly	Val
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Thr	Ala	Met	Leu	Leu	Ala	Cys	Lys	Tyr	Glu	Glu	Val	Ser	Val	Pro	Val
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Val	Glu	Asp	Leu	Val	Leu	Ile	Ser	Asp	Arg	Ala	Tyr	Thr	Lys	Gly	Gln
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Ile	Leu	Glu	Met	Glu	Lys	Leu	Ile	Leu	Asn	Thr	Leu	Gln	Phe	Asn	Met
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Ser	Val	Pro	Thr	Pro	Tyr	Val	Phe	Met	Lys	Arg	Phe	Leu	Lys	Ala	Ala
		290		295		300									
Asp	Ala	Asp	Lys	Gln	Leu	Glu	Leu	Ala	Ser	Phe	Phe	Met	Leu	Glu	Leu
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Cys	Leu	Val	Glu	Tyr	Gln	Met	Leu	Asn	Tyr	Arg	Pro	Ser	His	Leu	Ala
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Ala	Ala	Ala	Val	Tyr	Thr	Ala	Gln	Cys	Ala	Ile	Asn	Arg	Cys	Gln	His
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Trp	Thr	Lys	Val	Cys	Glu	Ser	His	Ser	Arg	Tyr	Thr	Ser	Asp	Gln	Leu
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Leu	Glu	Cys	Ser	Arg	Met	Met	Val	Asp	Phe	His	Gln	Lys	Ala	Gly	Thr
		370		375		380									
Ser	Lys	Leu	Thr	Gly	Val	His	Arg	Lys	Tyr	Ser	Thr	Tyr	Lys	Phe	Gly
		385		390		395									
Cys	Val	Ala	Lys	Ile	Leu	Pro	Ala	Gln	Phe	Leu	Leu	Glu	Ser	Gly	Gly
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Thr	Pro	Pro	Pro	Ser	Gly	Ala	Asn								
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<220>
 <221> primer_bind
 <222> (1)...(21)

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<220>
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 <222> (1)...(22)

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<220>
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<400> 6
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<210> 7
<211> 23
<212> DNA
<213> artificial organism

<220>
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<222> (1)...(23)

<400> 7
aatccacca gttgaatagg tcg
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<210> 8
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<212> DNA
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